SEQUENCE LISTING

- <110> Faustman, Denise L The General Hospital Corporation
- <120> TRANSPORTER PROTEIN SPLICE VARIANTS AND MODEL FOR IMMUNE DIVERSITY
- <130> seqlist-MGH-002.1 PCT (MGH-1247-1)

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<151> 1998-04-16

<160> 25

<170> PatentIn Ver. 2.0

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Ala Pro Trp Ser Trp Leu Leu Val Gly Tyr Gly Ala Ala Gly Leu Ser 100 105 110

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Ser Arg Pro Asp Leu Pro Leu Leu Val Ala Ala Phe Phe Leu Val 145 150 155 160

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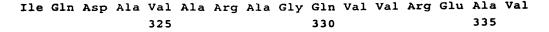
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- Gly Gly Leu Gln Thr Val Arg Ser Phe Gly Ala Glu Glu His Glu Val
- Cys Arg Tyr Lys Glu Ala Lys Glu Gln Cys Arg Gln Leu Tyr Trp Arg 355 360 365
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- Leu Trp Gly Leu Leu Lys Leu Arg Gly Leu Leu Gly Phe Val Gly Thr
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- Leu Ala Val Leu Gly Glu Thr Leu Ile Pro His Tyr Ser Gly Arg Val 165 170 175
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- Ile Gln Asp Ala Val Ala Arg Ala Gly Gln Val Val Arg Glu Ala Val
 325 330 335
- Gly Gly Leu Gln Thr Val Arg Ser Phe Gly Ala Glu Glu His Glu Val
- Cys Arg Tyr Lys Glu Ala Lys Glu Gln Cys Arg Gln Leu Tyr Trp Arg
- Arg Asp Leu Glu Arg Ala Leu Tyr Leu Leu Ile Arg Arg Val Leu His
- Leu Gly Val Gln Met Leu Met Leu Ser Cys Gly Leu Gln Gln Met Gln 385 390 395 400
- Asp Gly Glu Leu Thr Gln Gly Ser Leu Leu Ser Phe Met Ile Tyr Gln 405 410 415
- Glu Ser Val Gly Ser Tyr Val Gln Thr Leu Val Tyr Ile Tyr Gly Asp 420 425 430
- Met Leu Ser Asn Val Gly Ala Ala Glu Lys Val Phe Ser Tyr Met Asp
- Arg Gln Pro Asn Leu Pro Ser Pro Gly Thr Leu Ala Pro Thr Thr Leu

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Arg Asn Asn Ile Ala Tyr Gly Leu Gln Ser Cys Glu Asp Asp Lys Val 565 570 575

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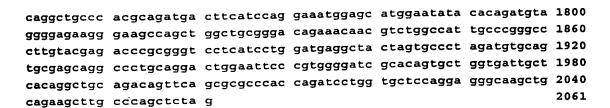
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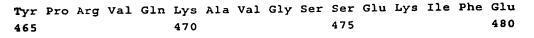
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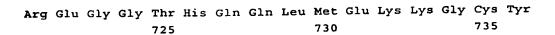
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- Gly Glu Ala Gln Lys Phe Arg Glu Lys Leu Gln Glu Ile Lys Thr Leu 385 390 395 400
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- Leu His Leu Glu Gly Leu Val Gln Phe Gln Asp Val Ser Phe Ala Tyr
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- Pro Asn Arg Pro Asp Val Leu Val Leu Gln Gly Leu Thr Phe Thr Leu 515 520 525
- Arg Pro Gly Glu Val Thr Ala Leu Val Gly Pro Asn Gly Ser Gly Lys
 530 535 540
- Ser Thr Val Ala Ala Leu Leu Gln Asn Leu Tyr Gln Pro Thr Gly Gly 545 550 555 560
- Gln Leu Leu Asp Gly Lys Pro Leu Pro Gln Tyr Glu His Arg Tyr
 565 570 575
- Leu His Arg Gln Val Ala Ala Val Gly Gln Glu Pro Gln Val Phe Gly 580 585 590
- Arg Ser Leu Gln Glu Asn Ile Ala Tyr Gly Leu Thr Gln Lys Pro Thr
 595 600 605
- Met Glu Glu Ile Thr Ala Ala Ala Val Lys Ser Gly Ala His Ser Phe 610 615 620
- Ile Ser Gly Leu Pro Gln Gly Tyr Asp Thr Glu Val Asp Glu Ala Gly 625 630 635 640
- Ser Gln Leu Ser Gly Gly Gln Arg Gln Ala Val Ala Leu Ala Arg Ala 645 650 655
- Leu Ile Arg Lys Pro Cys Val Leu Ile Leu Asp Asp Ala Thr Ser Ala 660 665 670
- Leu Asp Ala Asn Ser Gln Leu Gln Val Glu Gln Leu Leu Tyr Glu Ser 675 680 685
- Pro Glu Arg Tyr Ser Arg Ser Val Leu Leu Ile Thr Gln His Leu Ser 690 695 700
- Leu Val Glu Gln Ala Asp His Ile Leu Phe Leu Glu Gly Gly Ala Ile 705 710 715 720



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- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:
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- <400> 20

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24

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- <400> 21

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- <212> DNA
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<400> 24

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Gly Ala Ser Leu Ala Trp Leu Gly Thr Val Leu Leu Leu Leu Ala Asp 20 25 30

Trp Val Leu Leu Arg Thr Ala Leu Pro Arg Ile Phe Ser Leu Leu Val

Pro Thr Ala Leu Pro Leu Leu Arg Val Trp Ala Val Gly Leu Ser Arg 50 55 60

Trp Ala Val Leu Trp Leu Gly Ala Cys Gly Val Leu Arg Ala Thr Val
65 70 75 80

Gly Ser Lys Ser Glu Asn Ala Gly Ala Gln Gly Trp Leu Ala Ala Leu 85 90 95

Lys Pro Leu Ala Ala Ala Leu Gly Leu Ala Leu Pro Gly Leu Ala Leu
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Phe Arg Glu Leu Ile Ser Trp Gly Ala Pro Gly Ser Ala Asp Ser Thr 115 120 125

Arg Leu Leu His Trp Gly Ser His Pro Thr Ala Phe Val Val Ser Tyr 130 135 140

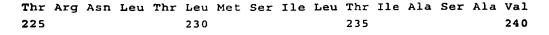
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Leu Val Val Leu Ser Ser Leu Gly Glu Met Ala Ile Pro Phe Phe Thr 195 200 205

Gly Arg Leu Thr Asp Trp Ile Leu Gln Asp Gly Ser Ala Asp Thr Phe 210 215 220



Leu Glu Phe Val Gly Asp Gly Ile Tyr Asn Asn Thr Met Gly His Val
245 250 255

His Ser His Leu Gln Gly Glu Val Phe Gly Ala Val Leu Arg Gln Glu 260 265 270

Thr Glu Phe Phe Gln Gln Asn Gln Thr Gly Asn Ile Met Ser Arg Val 275 280 285

Thr Glu Asp Thr Ser Thr Leu Ser Asp Ser Leu Ser Glu Asn Leu Ser 290 295 300

Leu Phe Leu Trp Tyr Leu Val Arg Gly Leu Cys Leu Leu Gly Ile Met 305 310 315 320

Leu Trp Gly Ser Val Ser Leu Thr Met Val Thr Leu Ile Thr Leu Pro 325 330 335

Leu Leu Phe Leu Leu Pro Lys Lys Val Gly Lys Trp Tyr Gln Leu Leu 340 345 350

Glu Val Gln Val Arg Glu Ser Leu Ala Lys Ser Ser Gln Val Ala Ile 355 360 365

Glu Ala Leu Ser Ala Met Pro Thr Val Arg Ser Phe Ala Asn Glu Glu 370 375 380

Gly Glu Ala Gln Lys Phe Arg Glu Lys Leu Gln Glu Ile Lys Thr Leu 385 390 395 400

Asn Gln Lys Glu Ala Val Ala Tyr Ala Val Asn Ser Trp Thr Thr Ser 405 410 415

Ile Ser Gly Met Leu Leu Lys Val Gly Ile Leu Tyr Ile Gly Gly Gln
420 425 430

Leu Val Thr Ser Gly Ala Val Ser Ser Gly Asn Leu Val Thr Phe Val
435 440 445

Leu Tyr Gln Met Gln Phe Thr Gln Ala Val Glu Val Leu Leu Ser Ile 450 455 460

Tyr Pro Arg Val Gln Lys Ala Val Gly Ser Ser Glu Lys Ile Phe Glu 465 470 475 480

Tyr Leu Asp Arg Thr Pro Arg Cys Pro Pro Ser Gly Leu Leu Thr Pro
485 490 495

Leu His Leu Glu Gly Leu Val Gln Phe Gln Asp Val Ser Phe Ala Tyr 500 505 510

Pro Asn Arg Pro Asp Val Leu Val Leu Gln Gly Leu Thr Phe Thr Leu 515 520 525

Arg Pro Gly Glu Val Thr Ala Leu Val Gly Pro Asn Gly Ser Gly Lys 530 535 540

Ser Thr Val Ala Ala Leu Leu Gln Asn Leu Tyr Gln Pro Thr Gly Gly 545 550 555 560

Gln Leu Leu Leu Asp Gly Lys Pro Leu Pro Gln Tyr Glu His Arg Tyr 565 570 575

Leu His Arg Gln Val Trp Lys Gln Val Ala 580 585